

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: _____

Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(a) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

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For PatentIn software help, call (703) 308-6856

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A Declosure

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1644

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000
TIME: 15:48:42

Input Set : A:\5647015.app
Output Set: N:\CRF3\05092000\H881509C.raw

5 (1) GENERAL INFORMATION:
C--> 7 (i) APPLICANT: SCHENDEL, Dolores J.
C--> 9 (ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA
C--> 11 (iii) NUMBER OF SEQUENCES: 45
C--> 13 (iv) CORRESPONDENCE ADDRESS:
C--> 14 (A) ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP
C--> 15 (B) STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby
C--> 16 (C) CITY: Washington
C--> 17 (D) STATE: DC
C--> 18 (E) COUNTRY: USA
C--> 19 (F) ZIP: 20005-5701
C--> 21 (v) COMPUTER READABLE FORM:
C--> 22 (A) MEDIUM TYPE: Floppy disk
C--> 23 (B) COMPUTER: IBM PC compatible
C--> 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
C--> 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
C--> 27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/08/881,509C
C--> 29 (B) FILING DATE: 24-Jun-1997
C--> 30 (C) CLASSIFICATION:
C--> 32 (viii) ATTORNEY/AGENT INFORMATION:
C--> 33 (A) NAME: Kitts, Monica Chin
C--> 34 (B) REGISTRATION NUMBER: 36,105
C--> 35 (C) REFERENCE/DOCKET NUMBER: 564-7015
C--> 37 (ix) TELECOMMUNICATION INFORMATION:
C--> 38 (A) TELEPHONE: (202) 638-5000
C--> 39 (B) TELEFAX: (202) 638-4810
42 (2) INFORMATION FOR SEQ ID NO: 1:
C--> 44 (i) SEQUENCE CHARACTERISTICS:
C--> 45 (A) LENGTH: 1341 base pairs
C--> 46 (B) TYPE: nucleic acid
C--> 47 (C) STRANDEDNESS: both
C--> 48 (D) TOPOLOGY: linear
C--> 50 (ix) FEATURE:
C--> 51 (A) NAME/KEY: CDS
C--> 52 (B) LOCATION: 1..801
C--> 54 (ix) FEATURE:
C--> 55 (A) NAME/KEY: sig_peptide
C--> 56 (B) LOCATION: 1..54
C--> 58 (ix) FEATURE:
C--> 59 (A) NAME/KEY: mat_peptide
C--> 60 (B) LOCATION: 55..801
C--> 62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 ATG AGG CAA GTG GCG AGA GTG ATC GTG TTC CTG ACC CTG AGT ACT TTG
65 Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
66 -18 -15 -10 -5
68 AGC CTT GCT AAG ACC ACC CAG CCC ATC TCC ATG GAC TCA TAT GAA GGA

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48

96

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000

TIME: 15:48:42

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Output Set: N:\CRF3\05092000\H881509C.raw

69 Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly	
70 1 5 10	
72 CAA GAA GTG AAC ATA ACC TGT AGC CAC AAC AAC ATT GCT ACA AAT GAT	144
73 Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp	
74 15 20 25 30	
76 TAT ATC ACG TGG TAC CAA CAG TTT CCC AGC CAA GGA CCA CGA TTT ATT	192
77 Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gin Gly Pro Arg Phe Ile	
78 35 40 45	
80 ATT CAA GGA TAC AAG ACA AAA GTT ACA AAC GAA GTG GCC TCC CTG TTT	240
81 Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe	
82 50 55 60	
84 ATC CCT GCC GAC AGA AAG TCC AGC ACT CTG AGC CTG CCC CGG GTT TCC	288
85 Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser	
86 65 70 75	
88 CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GGT GGT TCT GCA AGG	336
89 Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg	
90 80 85 90	
92 CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC	384
93 Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile	
94 95 100 105 110	
96 CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT	432
97 Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser	
98 115 120 125	
100 GAC AAG TCT GTC CTA TTC ACC GAT TTT GAT TCT CAA ACA AAT GTG	480
101 Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val	
102 130 135 140	
104 TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA	528
105 Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu	
106 145 150 155	
108 GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC	576
109 Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser	
110 150 165 170	
112 AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT	624
113 Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile	
114 175 180 185 190	
116 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG	672
117 Pro Glu Asp Thr Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys	
118 195 200 205	
120 CTG GTC GAG AAA AGC TTT GAA ACA GAT ACG AAC CTA AAC TTT CAA AAC	720
121 Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn	
122 210 215 220	
124 CTG TCA GTG ATT GGG TTC CGA ATC CTC CTC CTG AAA GTG GCC GGG TTT	768
125 Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Lys Val Ala Gly Phe	
126 225 230 235	
128 AAT CTG CTC ATG ACG CTG CGG CTG TGG TCC AGC TGAGATCTGC AAGATTGTAA	821
129 Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser	
130 240 245	
132 GACAGCCTGT GCTCCCTCGC TCCTTCCTCT GCATTGCCCT TCTTCTCCCT CTCCAAACAG	881
134 AGGGAACTCT CCTACCCCCA AGGAGGTGAA AGCTGCTACC ACCTCTGTGC CCCCCCGGCA	941

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/881,509C

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Input Set : A:\5647015.app

Output Set: N:\CRF3\05092000\H881509C.raw

136	ATGCCACCAA	CTGGATCCTA	CCCGAATTAA	TGATTAAGAT	TGCTGAAGAG	CTGCCAAACA
138	CTGCTGCCAC	CCCCTCTGTT	CCCTTATTGC	TGCTTGTCAC	TGCCTGACAT	TCACGGCAGA
140	GGCAAGGCTG	CCGCAGCCTC	CCCTGGCTGT	GCACATTCCC	TCCCTGCTCC	CAGAGACTGC
142	CTCCCCCATC	CCACAGATGA	TGGATCTCA	GTGGGTTCTC	TTGGGCTCTA	GGTCCTGGAG
144	AATGTTGTGA	GGGGTTTATT	TTTTTTAAAT	AGTGTTCATA	AAGAAATACA	TAGTATTCTT
146	CTTCTCAAGA	CGTGGGGGGA	AATTATCTCA	TTATCGAGGC	CCTGCTATGC	TGTGTGTCTG
148	GCGGTGTTGT	ATGTCCTGCT	GCCGATGCCT	TCATTAAT		

1001

1061

1121

1181

1241

1301

1341

151 (2) INFORMATION FOR SEQ ID NO: 2:

C--> 153 (i) SEQUENCE CHARACTERISTICS:

C--> 154 (A) LENGTH: 267 amino acids

C--> 155 (B) TYPE: amino acid

C--> 156 (D) TOPOLOGY: linear

C--> 158 (ii) MOLECULE TYPE: protein

C--> 160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

162	Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu					
163	-18	-15	-10	-5		
165	Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly	1	5	10		
166						
168	Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp					
169	15	20	25	30		
171	Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile	35	40	45		
172						
174	Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe	50	55	60		
175						
177	Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser	65	70	75		
178						
180	Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg	80	85	90		
181						
183	Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile	95	100	105	110	
184						
186	Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser	115	120	125		
187						
189	Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val	130	135	140		
190						
192	Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu	145	150	155		
193						
195	Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser	160	165	170		
196						
198	Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile	175	180	185	190	
199						
201	Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys	195	200	205		
202						
204	Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn	210	215	220		
205						
207	Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe	225	230	235		
208						
210	Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser	240	245			
211						

214 (2) INFORMATION FOR SEQ ID NO: 3:

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000
TIME: 15:48:42Input Set : A:\5647015.app
Output Set: N:\CRF3\05092000\H881509C.raw

C--> 216 (i) SEQUENCE CHARACTERISTICS:
 C--> 217 (A) LENGTH: 936 base pairs
 C--> 218 (B) TYPE: nucleic acid
 C--> 219 (C) STRANDEDNESS: both
 C--> 220 (D) TOPOLOGY: linear
 C--> 222 (ix) FEATURE:
 C--> 223 (A) NAME/KEY: CDS
 C--> 224 (B) LOCATION:1..933
 C--> 226 (ix) FEATURE:
 C--> 227 (A) NAME/KEY: sig_peptide
 C--> 228 (B) LOCATION:1..63
 C--> 230 (ix) FEATURE:
 C--> 231 (A) NAME/KEY: mat_peptide
 C--> 232 (B) LOCATION:64..933
 C--> 234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 236 ATG GAT ACC TGG CTC GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA 48
 237 Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
 238 -21 -20 -15 -10
 240 GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA 96
 241 Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
 242 -5 1 5 10
 244 CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC 144
 245 Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
 246 15 20 25
 248 TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT 192
 249 Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe
 250 30 35 40
 252 CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC 240
 253 Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
 254 45 50 55
 256 GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG 288
 257 Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
 258 60 65 70 75
 260 AAG ATC CCG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC 336
 261 Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala
 262 80 85 90
 264 AGC AGC GAA ACT AAC TCC TAC GAG CAG TAC TTC GGG CCG GGC ACC AGG 384
 265 Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
 266 95 100 105
 268 CTC ACG GTC ACA GAG GAC CTG AAA AAC GTG TTC CCA CCC GAG GTC GCT 432
 269 Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
 270 110 115 120
 272 GTG TTT GAG CCA TCA GAA GCA GAG ATC TCC CAC ACC CAA AAG GCC ACA 480
 273 Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
 274 125 130 135
 276 CTG GTG TGC CTG GCC ACA GGC TTC TAC CCC GAC CAC GTG GAG CTG AGC 528
 277 Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
 278 140 145 150 155
 280 TGG TGG GTG AAT GGG AAG GAG GTG CAC AGT GGG GTC AGC ACA GAC CCG 576

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/881,509C

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Input Set : A:\5647015.app
Output Set: N:\CRF3\05092000\H881509C.raw

281	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro
282					160				165							170
284	CAG	CCC	CTC	AAG	GAG	CAG	CCC	GCC	CTC	AAT	GAC	TCC	AGA	TAC	TGC	CTG
285	Gln	Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu
286					175				180							185
288	AGC	AGC	CGC	CTG	AGG	GTC	TCG	GCC	ACC	TTC	TGG	CAG	AAC	CCC	CGC	AAC
289	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn
290					190				195							200
292	CAC	TTC	CGC	TGT	CAA	GTC	CAG	TTC	TAC	GGG	CTC	TCG	GAG	AAT	GAC	GAG
293	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu
294					205				210							215
296	TGG	ACC	CAG	GAT	AGG	GCC	AAA	CCT	GTC	ACC	CAG	ATC	GTC	AGC	GCC	GAG
297	Trp	Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu
298					220				225							235
300	GCC	TGG	GGT	AGA	GCA	GAC	TGT	GGC	TTC	ACC	TCC	GAG	TCT	TAC	CAG	CAA
301	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln
302					240				245							250
304	GGG	GTC	CTG	TCT	GCC	ACC	ATC	CTC	TAT	GAG	ATC	TTG	CTA	GGG	AAG	GCC
305	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Gly	Lys	Ala	
306					255				260							265
308	ACC	TTG	TAT	GCC	GTG	CTG	GTC	AGT	GCC	CTC	GTG	CTG	ATG	GCC	ATG	GTC
309	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val
310					270				275							280
312	AAG	AGA	AAG	GAT	TCC	AGA	GGC	TAG								
313	Lys	Arg	Lys	Asp	Ser	Arg	Gly									
314					285				290							
317	(2)	INFORMATION FOR SEQ ID NO: 4:														
C-->	319	(i) SEQUENCE CHARACTERISTICS:														
C-->	320	(A) LENGTH: 311 amino acids														
C-->	321	(B) TYPE: amino acid														
C-->	322	(D) TOPOLOGY: linear														
C-->	324	(ii) MOLECULE TYPE: protein														
C-->	326	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:														
328	Met	Asp	Thr	Trp	Leu	Val	Cys	Trp	Ala	Ile	Phe	Ser	Leu	Leu	Lys	Ala
329	-21	-20					-15						-10			
331	Gly	Leu	Thr	Glu	Pro	Glu	Val	Thr	Gln	Thr	Pro	Ser	His	Gln	Val	Thr
332	-5						1			5						10
334	Gln	Met	Gly	Gln	Glu	Val	Ile	Leu	Arg	Cys	Val	Pro	Ile	Ser	Asn	His
335							15			20						25
337	Leu	Tyr	Phe	Tyr	Trp	Tyr	Arg	Gln	Ile	Leu	Gly	Gln	Lys	Val	Glu	Phe
338							30			35						40
340	Leu	Val	Ser	Phe	Tyr	Asn	Asn	Glu	Ile	Ser	Glu	Lys	Ser	Glu	Ile	Phe
341							45			50						55
343	Asp	Asp	Gln	Phe	Ser	Val	Glu	Arg	Pro	Asp	Gly	Ser	Asn	Phe	Thr	Leu
344							60			65						75
346	Lys	Ile	Arg	Ser	Thr	Lys	Leu	Glu	Asp	Ser	Ala	Met	Tyr	Phe	Cys	Ala
347							80			85						90
349	Ser	Ser	Glu	Thr	Asn	Ser	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg
350							95			100						105

VERIFICATION SUMMARY
 PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000
 TIME: 15:48:43

Input Set : A:\5647015.app
 Output Set: N:\CRF3\05092000\H881509C.raw

L:7 M:220 C: Keyword misspelled, [(i) APPLICANT:]
 L:9 M:220 C: Keyword misspelled, [(ii) TITLE OF INVENTION:]
 L:11 M:220 C: Keyword misspelled, [(iii) NUMBER OF SEQUENCES:]
 L:13 M:220 C: Keyword misspelled, [(iv) CORRESPONDENCE ADDRESS:]
 L:14 M:220 C: Keyword misspelled, [(A) ADDRESSEE:]
 L:15 M:220 C: Keyword misspelled, [(B) STREET:]
 L:16 M:220 C: Keyword misspelled, [(C) CITY:]
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 L:18 M:220 C: Keyword misspelled, [(E) COUNTRY:]
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 L:22 M:220 C: Keyword misspelled, [(A) MEDIUM TYPE:]
 L:23 M:220 C: Keyword misspelled, [(B) COMPUTER:]
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 L:25 M:220 C: Keyword misspelled, [(D) SOFTWARE:]
 L:27 M:220 C: Keyword misspelled, [(vi) CURRENT APPLICATION DATA:]
 L:28 M:220 C: Keyword misspelled, [(A) APPLICATION NUMBER:]
 L:29 M:220 C: Keyword misspelled, [(B) FILING DATE:]
 L:30 M:220 C: Keyword misspelled, [(C) CLASSIFICATION:]
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 L:45 M:220 C: Keyword misspelled, [(A) LENGTH:]
 L:46 M:220 C: Keyword misspelled, [(B) TYPE:]
 L:47 M:220 C: Keyword misspelled, [(C) STRANDEDNESS:]
 L:48 M:220 C: Keyword misspelled, [(D) TOPOLOGY:]
 L:50 M:220 C: Keyword misspelled, [(ix) FEATURE:]
 L:51 M:220 C: Keyword misspelled, [(A) NAME/KEY:]
 L:52 M:220 C: Keyword misspelled, [(B) LOCATION:]
 L:54 M:220 C: Keyword misspelled, [(ix) FEATURE:]
 L:55 M:220 C: Keyword misspelled, [(A) NAME/KEY:]
 L:56 M:220 C: Keyword misspelled, [(B) LOCATION:]
 L:58 M:220 C: Keyword misspelled, [(ix) FEATURE:]
 L:59 M:220 C: Keyword misspelled, [(A) NAME/KEY:]
 L:60 M:220 C: Keyword misspelled, [(B) LOCATION:]
 L:62 M:220 C: Keyword misspelled, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:153 M:220 C: Keyword misspelled, [(i) SEQUENCE CHARACTERISTICS:]
 L:154 M:220 C: Keyword misspelled, [(A) LENGTH:]
 L:155 M:220 C: Keyword misspelled, [(B) TYPE:]
 L:156 M:220 C: Keyword misspelled, [(D) TOPOLOGY:]
 L:158 M:220 C: Keyword misspelled, [(ii) MOLECULE TYPE:]
 L:160 M:220 C: Keyword misspelled, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:216 M:220 C: Keyword misspelled, [(i) SEQUENCE CHARACTERISTICS:]

VERIFICATION SUMMARY

PATENT APPLICATION: US/08/881,509C

DATE: 05/09/2000

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Input Set : A:\5647015.app
Output Set: N:\CRF3\05092000\H881509C.raw

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L:218 M:220 C: Keyword misspelled, [(B) TYPE:]
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L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:473 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:507 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:541 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:575 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:609 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:643 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:693 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23, Value=[not relevant]
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:715 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24, Value=[not relevant]
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:737 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25, Value=[not relevant]
L:749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:759 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26, Value=[not relevant]
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:781 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27, Value=[not relevant]
L:797 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=28, Value=[not relevant]
L:813 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=29, Value=[not relevant]
L:829 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=30, Value=[not relevant]
L:845 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=31, Value=[not relevant]
L:861 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32, Value=[not relevant]
L:877 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=33, Value=[not relevant]
L:893 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=34, Value=[not relevant]
L:909 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=35, Value=[not relevant]
L:925 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=36, Value=[not relevant]
L:941 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=37, Value=[not relevant]
L:957 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=38, Value=[not relevant]
L:973 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=39, Value=[not relevant]
L:989 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=40, Value=[not relevant]
L:1005 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=41, Value=[not relevant]
L:1021 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=42, Value=[not relevant]
L:1037 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=43, Value=[not relevant]
L:1053 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=44, Value=[not relevant]
L:1068 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=45, Value=[not relevant]
L:1080 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45